

General Description References Links Keywords Sequence

**General information**

www.uniprot.org **Q12563**  
 Entry name **Q12563**  
 Accession number **Q12563**  
 Created TrEMBLrel. 01, 1-NOV-1996  
 Sequence update TrEMBLrel. 01, 1-NOV-1996  
 Annotation update TrEMBLrel. 25, 1-OCT-2003

**Description and origin of the Protein**

Description Alpha-mannosidase (EC 3.2.1.113).  
 Organism source *Aspergillus phoenicis*.  
 Taxonomy Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Aspergillus.  
 NCBI TaxID 5063

**References**

- [1] Inoue,T., Yoshida,T., Ichishima,E.,  
**Molecular cloning and nucleotide sequence of the 1,2-alpha-D- mannosidase gene of *Aspergillus saitoi* and expression of the gene in yeast cells.**  
 (1995) *Biochim. Biophys. Acta* **1253**:141-145  
 Position SEQUENCE FROM N.A.  
 Medline 96106423  
 PubMed 8519794

**Database cross-references**

EMBL D49827; BAA08634.1; -.  
 HSSP P31723; 1KRE.  
 GO GO:0016020; C:membrane; IEA.  
GO:0005509; F:calcium ion binding; IEA.  
GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
GO:0004571; F:mannosyl-oligosaccharide 1,2-alpha-mannosid...; IEA.  
GO:0005975; P:carbohydrate metabolism; IEA.  
GO:0006487; P:N-linked glycosylation; IEA.  
 InterPro IPR001382; Glyco\_hydro\_47.  
 Pfam PF01532; Glyco\_hydro\_47; 1.  
 PRINTS PR00747; GLYHDLASE47.  
 ProDom PD003239; Glyco\_hydro\_47; 1.

**Keywords**

Glycosidase; Hydrolase;

**Sequence information**

Length: **513 aa**, molecular weight: **55874 Da**, CRC64 checksum: **0FDAB2CB27E93724**

MHLPSLSLSL	TALAIASPSA	AYPHFGSSQP	VLHSSSDTTQ	SRADAIKAAF	SHAWDGYLQY	60
AFPHDELHPV	SNGYGDSRNG	WGASAVDALS	TAVIMRNATI	VNQILDHVGK	IDYSKTNTTV	120
SLFETTIRYL	GGMLSGYDLL	KGPVSDLVQN	SSKIDVLLTQ	SKNLADVLKF	AFDTPSGVPY	180
NNLNITSGGN	DGAKTNGLAV	TGTLALEWTR	LSDLTGDDTY	ADLSQKAESY	LLNPQPKSAE	240
PFPGLVGSNI	NISNGQFTDA	QVSWNGGDDS	YYEYLIKMYV	YDPKREGLYK	DRWVAAAQST	300
MQHLASHPSS	RPDLTFLASY	NNGTLGLSSQ	HLTCFDGGSF	LLGGTVLNRT	DFINFGLDLV	360
SGCHDTYNST	LTGIGPESFS	WDTSDIPSSQ	QSLYEKAGFY	ITSGAYILRP	EVIESFYIYAW	420
RVTGQETYRD	WIWSAFSAVN	DYCRTSSGFS	GLTDVNAANG	GSRYDNQESF	LFAEVMKYSY	480
MAFAEDAAWQ	VQPGSGNQFV	FNTEAHPVRV	SST			513

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